

1/1

1 atgctcctgctgctggccgaataacctgcaacagttctacaagggttcggcgtcttccag 60
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 61 tacctgacctgcgccgattctcagcgtgctcaccgcgctgtcgctgtcgctgtggctg 120
 TyrLeuThrLeuArgGlyIleLeuSerValLeuThrAlaLeuSerLeuSerLeuTrpLeu
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 ValLeuValValThrLeuLeuPheGlyAlaIleGlyTrpValAspAspTyrArgLysVal
 361 atcgagaagaactcccggtggcctgccgagccgctggaagtacttctggcagtcgggtgttc 420
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 TyrPheValIleValGlySerSerAsnAlaValAsnLeuThrAspGlyLeuAspGlyLeu
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 661 aacgtgaagtccgccgagtacctgctgattcccaacgtaccgggcccggcgagctgac 720
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 721 gtgttctgcgccgctggtcgccgcccgcctcggttctctggttcaacacctatccg 780
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 1081 tga 1140

FIG. 1